heterozygosity rate of at least about 0.18 and having a mean inter-marker spacing of less than 50kb.

Please add the following new claim:

122. (New) A map produced by the method of Claim 86.

REMARKS

Status of the claims

Claims 86, 88, 89, and 92-105 are currently pending and are under examination. In the Office Action dated January 22, 2002, each of these claims has been rejected under either 35 U.S.C. §102(b) or §103(a). With entry of the present amendment, claim 86 has been amended. Support for the present amendment can be found, *inter alia*, at page 25, lines 8-11 of the specification as filed. No new matter has been added.

Rejections under 35 U.S.C. §102(b)/ 103(a)

In the Office Action, claims 86, 88, 89, and 92-105 were rejected as allegedly anticipated by, or alternatively obvious in view of, Goelet, et al. (WO 95/12607; "Goelet"). As discussed below, the presently-claimed invention provides a specific method, comprising four steps, of selectively obtaining sets of single nucleotide polymorphisms (SNPs) with desired properties, e.g., with a specified minimum heterozygosity and maximum inter-marker spacing. The cited reference, Goelet, describes a method of randomly selecting genomic clones and identifying SNPs within the clones. According to the Examiner, even though Goelet fails to address the heterozygosity and inter-marker spacing of markers obtained using their method, this reference could be "fairly" scaled up to identify every SNP of any animal. Consequently, because a collection including every SNP in the genome would meet both the heterozygosity and inter-marker spacing limitations of the present claims, the method of Goelet inherently anticipates or renders obvious the present claims. Applicants respectively amend-in-part and traverse-in-part.

To fully appreciate the present invention, it is important to recognize that, at the time of the invention, researchers faced significant technical challenges in identifying collections of SNPs that could be used for genetic association analyses. While previously-known markers, such as RFLPs or microsatellites, were useful for segregation analyses, they could not be used for association analyses because of their inadequate inter-marker spacing, distribution within the genome, and ease of use (see, e.g., page 13, line 15,